

## SEQUENCE LISTING

<110> Lee, Se-Jin  
McPherron, Alexandra C.

<120> PROMYOSTATIN PEPTIDES AND METHODS OF  
USING SAME

<130> JHU1120-11

<150> 09/124,180

<151> 1998-07-28

<150> 09/019,070

<151> 1998-02-05

<150> 08/862,445

<151> 1997-05-23

<150> 08/847,910

<151> 1997-04-28

<150> 08/795,071

<151> 1997-02-05

<150> 08/525,596

<151> 1995-10-26

<160> 29

<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (59)...(1183)

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Met Gln Lys Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile

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5

10

15

gtt gct ggt cca gtg gat cta aat gag aac agt gag caa aaa gaa aat 154

Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn

20

25

30

gtg gaa aaa gag ggg ctg tgt aat gca tgt act tgg aga caa aac act 202

Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr

35

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45

aaa tct tca aga ata gaa gcc att aag ata caa atc ctc agt aaa ctt 250

Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu

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55

60

cgt ctg gaa aca gct cct aac atc agc aaa gat gtt ata aga caa ctt	298
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu	
65 70 75 80	
tta ccc aaa gct cct cca ctc cgg gaa ctg att gat cag tat gat gtc	346
Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val	
85 90 95	
cag agg gat gac agc agc gat ggc tct ttg gaa gat gac gat tat cac	394
Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His	
100 105 110	
gct aca acg gaa aca atc att acc atg cct aca gag tct gat ttt cta	442
Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu	
115 120 125	
atg caa gtg gat gga aaa ccc aaa tgt tgc ttc ttt aaa ttt agc tct	490
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Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu	
145 150 155 160	
aga ccc gtc gag act cct aca aca gtg ttt gtg caa atc ctg aga ctc	586
Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu	
165 170 175	
atc aaa cct atg aaa gac ggt aca agg tat act gga atc cga tct ctg	634
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu	
180 185 190	
aaa ctt gac atg aac cca ggc act ggt att tgg cag agc att gat gtg	682
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val	
195 200 205	
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Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly	
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att gaa ata aaa gct tta gat gag aat ggt cat gat ctt gct gta acc	778
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr	
225 230 235 240	
ttc cca gga cca gga gaa gat ggg ctg aat ccg ttt tta gag gtc aag	826
Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys	
245 250 255	
gta aca gac aca cca aaa aga tcc aga agg gat ttt ggt ctt gac tgt	874
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys	
260 265 270	
gat gag cac tca aca gaa tca cga tgc tgt cgt tac cct cta act gtg	922
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val	
275 280 285	
gat ttt gaa gct ttt gga tgg gat tgg att atc gct cct aaa aga tat	970
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr	
290 295 300	

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 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys  
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tat cct cat act cat ctg gta cac caa gca aac ccc aga ggt tca gca 1066  
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala  
 325 330 335

ggc cct tgc tgt act ccc aca aag atg tct cca att aat atg cta tat 1114  
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr  
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 Val Asp Arg Cys Gly Cys Ser  
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<211> 375

<212> PRT

<213> Homo sapiens

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 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr  
 35 40 45  
 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu

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Arg Leu Glu Thr Ala	Pro Asn Ile Ser Lys Asp	Val Ile Arg Gln Leu
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Gln Arg Asp Asp Ser	Ser Asp Gly Ser Leu Glu Asp	Asp Asp Tyr His
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Ala Thr Thr Glu Thr	Ile Ile Thr Met Pro Thr Glu	Ser Asp Phe Leu
	115	120
Met Gln Val Asp Gly	Lys Pro Lys Cys Cys Phe Phe	Lys Phe Ser Ser
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Lys Ile Gln Tyr Asn	Lys Val Val Lys Ala Gln Leu	Trp Ile Tyr Leu
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Arg Pro Val Glu Thr	Pro Thr Thr Val Phe Val Gln	Ile Leu Arg Leu
	165	170
Ile Lys Pro Met Lys	Asp Gly Thr Arg Tyr Thr Gly	Ile Arg Ser Leu
	180	185
Lys Leu Asp Met Asn	Pro Gly Thr Gly Ile Trp Gln	Ser Ile Asp Val
	195	200
Lys Thr Val Leu Gln	Asn Trp Leu Lys Gln Pro Glu	Ser Asn Leu Gly
	210	215
Ile Glu Ile Lys Ala	Leu Asp Glu Asn Gly His Asp	Leu Ala Val Thr
225	230	235
Phe Pro Gly Pro Gly	Glu Asp Gly Leu Asn Pro Phe	Leu Glu Val Lys
	245	250
Val Thr Asp Thr Pro	Lys Arg Ser Arg Arg Asp Phe	Gly Leu Asp Cys
	260	265
Asp Glu His Ser Thr	Glu Ser Arg Cys Cys Arg Tyr	Pro Leu Thr Val
	275	280
Asp Phe Glu Ala Phe	Gly Trp Asp Trp Ile Ile Ala	Pro Lys Arg Tyr
	290	295
Lys Ala Asn Tyr Cys	Ser Gly Glu Cys Glu Phe Val	Phe Leu Gln Lys
305	310	315
Tyr Pro His Thr His	Leu Val His Gln Ala Asn Pro	Arg Gly Ser Ala
	325	330
Gly Pro Cys Cys Thr	Pro Thr Lys Met Ser Pro Ile	Asn Met Leu Tyr
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Phe Asn Gly Lys Glu	Gln Ile Ile Tyr Gly Lys Ile	Pro Ala Met Val
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Val Asp Arg Cys Gly	Cys Ser	
370	375	

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&lt;211&gt; 2676

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

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ctg	caa	atg	tat	gtt	tat	att	tac	ctg	ttc	atg	ctg	att	gct	gct	ggc	163
Leu	Gln	Met	Tyr	Val	Tyr	Ile	Tyr	Leu	Phe	Met	Leu	Ile	Ala	Ala	Gly	
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cca	gtg	gat	cta	aat	gag	ggc	agt	gag	aga	gaa	gaa	aat	gtg	gaa	aaa	211
Pro	Val	Asp	Leu	Asn	Glu	Gly	Ser	Glu	Arg	Glu	Glu	Asn	Val	Glu	Lys	
			25					30						35		
gag	ggg	ctg	tgt	aat	gca	tgt	gcg	tgg	aga	caa	aac	acg	agg	tac	tcc	259
Glu	Gly	Leu	Cys	Asn	Ala	Cys	Ala	Trp	Arg	Gln	Asn	Thr	Arg	Tyr	Ser	
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aga	ata	gaa	gcc	ata	aaa	att	caa	atc	ctc	agt	aag	ctg	cgc	ctg	gaa	307
Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	Arg	Leu	Glu	
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aca	gct	cct	aac	atc	agc	aaa	gat	gct	ata	aga	caa	ctt	ctg	cca	aga	355
Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu	Leu	Pro	Arg	
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gcg	cct	cca	ctc	cgg	gaa	ctg	atc	gat	cag	tac	gac	gtc	cag	agg	gat	403
Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	Gln	Arg	Asp	
	85				90				95						100	
gac	agc	agt	gat	ggc	tct	ttg	gaa	gat	gac	gat	tat	cac	gct	acc	acg	451
Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	Ala	Thr	Thr	
				105					110					115		
gaa	aca	atc	att	acc	atg	cct	aca	gag	tct	gac	ttt	cta	atg	caa	gcg	499
Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu	Met	Gln	Ala	
			120					125					130			
gat	ggc	aag	ccc	aaa	tgt	tgc	ttt	ttt	aaa	ttt	agc	tct	aaa	ata	cag	547
Asp	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	Lys	Ile	Gln	
		135					140					145				
tac	aac	aaa	gta	gta	aaa	gcc	caa	ctg	tgg	ata	tat	ctc	aga	ccc	gtc	595
Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	Arg	Pro	Val	
	150					155					160					
aag	act	cct	aca	aca	gtg	ttt	gtg	caa	atc	ctg	aga	ctc	atc	aaa	ccc	643
Lys	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	Ile	Lys	Pro	
	165				170					175					180	
atg	aaa	gac	ggg	aca	agg	tat	act	gga	atc	cga	tct	ctg	aaa	ctt	gac	691
Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	Lys	Leu	Asp	
				185				190						195		
atg	agc	cca	ggc	act	ggg	att	tgg	cag	agt	att	gat	gtg	aag	aca	gtg	739
Met	Ser	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	Lys	Thr	Val	
		200						205					210			
ttg	caa	aat	tgg	ctc	aaa	cag	cct	gaa	tcc	aac	tta	ggc	att	gaa	atc	787
Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	Ile	Glu	Ile	
		215					220					225				
aaa	gct	ttg	gat	gag	aat	ggc	cat	gat	ctt	gct	gta	acc	ttc	cca	gga	835
Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr	Phe	Pro	Gly	
	230					235					240					
cca	gga	gaa	gat	ggg	ctg	aat	ccc	ttt	tta	gaa	gtc	aag	gtg	aca	gac	883
Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys	Val	Thr	Asp	
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aca ccc aag agg tcc cgg aga gac ttt ggg ctt gac tgc gat gag cac	931
Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys Asp Glu His	
265 270 275	
tcc acg gaa tcc cgg tgc tgc cgc tac ccc ctc acg gtc gat ttt gaa	979
Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu	
280 285 290	
gcc ttt gga tgg gac tgg att atc gca ccc aaa aga tat aag gcc aat	1027
Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn	
295 300 305	
tac tgc tca gga gag tgt gaa ttt gtg ttt tta caa aaa tat ccg cat	1075
Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys Tyr Pro His	
310 315 320	
act cat ctt gtg cac caa gca aac ccc aga ggc tca gca ggc cct tgc	1123
Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala Gly Pro Cys	
325 330 335 340	
tgc act ccg aca aaa atg tct ccc att aat atg cta tat ttt aat ggc	1171
Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe Asn Gly	
345 350 355	
aaa gaa caa ata ata tat ggg aaa att cca gcc atg gta gta gac cgc	1219
Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val Val Asp Arg	
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Cys Gly Cys Ser	
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&lt;210&gt; 4

&lt;211&gt; 376

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 4

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			20					25					30		
Asn	Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Ala	Trp	Arg	Gln	Asn
		35				40					45				
Thr	Arg	Tyr	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys
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Leu	Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln
65					70					75					80
Leu	Leu	Pro	Arg	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp
				85					90					95	
Val	Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr
			100					105					110		
His	Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe
		115						120					125		
Leu	Met	Gln	Ala	Asp	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser
	130					135					140				
Ser	Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr
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Leu	Arg	Pro	Val	Lys	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg
				165					170					175	
Leu	Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser
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Leu	Lys	Leu	Asp	Met	Ser	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp
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Val	Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu
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Gly	Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val
225					230					235					240
Thr	Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val
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Lys	Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp
			260					265					270		
Cys	Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr
		275					280					285			
Val	Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg
	290					295					300				
Tyr	Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln
305					310					315					320
Lys	Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser
				325					330					335	
Ala	Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu
			340					345					350		
Tyr	Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met
		355					360					365			
Val	Val	Asp	Arg	Cys	Gly	Cys	Ser								
	370					375									

&lt;210&gt; 5

&lt;211&gt; 1131

&lt;212&gt; DNA

&lt;213&gt; Rattus norvegicus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1128)

&lt;400&gt; 5

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att gct gct ggc cca gtg gat cta aat gag gac agt gag aga gag gcg	96
Ile Ala Ala Gly Pro Val Asp Leu Asn Glu Asp Ser Glu Arg Glu Ala	
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Asn Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn	
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aca agg tac tcc aga ata gaa gcc ata aaa att caa atc ctc agt aaa	192
Thr Arg Tyr Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys	
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ctc cgc ctg gaa aca gcg cct aac atc agc aaa gat gct ata aga caa	240
Leu Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln	
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Leu Leu Pro Arg Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp	
85 90 95	
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Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Tyr	
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cac gct acc acg gaa aca atc att acc atg cct acc gag tct gac ttt	384
His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe	
115 120 125	
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Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser	
130 135 140	
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Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr	
145 150 155 160	
ctg aga gcc gtc aag act cct aca aca gtg ttt gtg caa atc ctg aga	528
Leu Arg Ala Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg	
165 170 175	
ctc atc aaa ccc atg aaa gac ggt aca agg tat acc gga atc cga tct	576
Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser	
180 185 190	
ctg aaa ctt gac atg agc cca ggc act ggt att tgg cag agt att gat	624
Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp	
195 200 205	
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Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu	
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ggc att gaa atc aaa gct ttg gat gag aat ggg cat gat ctt gct gta	720



Gly 225	Ile	Glu	Ile	Lys	Ala 230	Leu	Asp	Glu	Asn	Gly 235	His	Asp	Leu	Ala	Val 240	
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Thr Phe Pro Gly				Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	
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aaa gta aca gac aca ccc aag agg tcc cgg aga gac ttt ggg ctt gac																816
Lys Val Thr		Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp		
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tgc gat gaa cac tcc acg gaa tcg cgg tgc tgt cgc tac ccc ctc acg																864
Cys Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr		
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Val Asp Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg			
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Tyr Lys Ala Asn Tyr				Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln		
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Lys Tyr Pro His Thr				His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser		
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Ala Gly Pro Cys Cys Thr Pro Thr				Lys	Met	Ser	Pro	Ile	Asn	Met	Leu					
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Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met																
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Val Val Asp Arg Cys Gly Cys Ser																
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 <212> PRT  
 <213> Rattus norvegicus

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 Thr Arg Tyr Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys  
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 Leu Leu Pro Arg Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp  
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 Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr  
 100 105 110

His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe  
 115 120 125  
 Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser  
 130 135 140  
 Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr  
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 Leu Arg Ala Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg  
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 Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser  
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 Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp  
 195 200 205  
 Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu  
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 Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val  
 225 230 235 240  
 Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val  
 245 250 255  
 Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp  
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 Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr  
 275 280 285  
 Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg  
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 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln  
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 Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser  
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 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu  
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 Val Val Asp Arg Cys Gly Cys Ser  
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<220>  
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 Ala Val Asp Pro Val Ala Leu Asp Gly Ser Ser Gln Pro Thr Glu Asn  
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 Ala Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr  
 35 40 45  
 aaa tcc tcc aga ata gaa gcc ata aaa att caa atc ctc agc aaa ctg 192  
 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu  
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Leu	Pro	Lys	Ala	Pro	Pro	Leu	Gln	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	
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Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	
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gcc	aca	acc	gag	acg	att	atc	aca	atg	cct	acg	gag	tct	gat	ttt	ctt	384
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu	
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gta	caa	atg	gag	gga	aaa	cca	aaa	tgt	tgc	ttc	ttt	aag	ttt	agc	tct	432
Val	Gln	Met	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	
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Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	
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Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	
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Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Arg	
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Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	
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Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	
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Glu	Lys	Asp	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	Gln	Asn	Thr	Lys
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Leu	Glu	Gln	Ala	Pro	Asn	Ile	Ser	Arg	Asp	Val	Ile	Lys	Gln	Leu	Leu
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Pro	Lys	Ala	Pro	Pro	Leu	Gln	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	Gln
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Gln	Val	Gln	Lys	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	Ile
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Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	Lys
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Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Arg	Val
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 Glu His Ser Thr Glu Ser Arg Cys Arg Tyr Pro Leu Thr Val Asp  
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 Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys  
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 Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys Tyr  
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 Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala Gly  
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 Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe  
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 Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val Val  
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 Asp Arg Cys Gly Cys Ser  
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&lt;211&gt; 1128

&lt;212&gt; DNA

&lt;213&gt; Baboon

&lt;220&gt;

&lt;221&gt; CDS

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Val	Ala	Gly	Pro	Val	Asp	Leu	Asn	Glu	Asn	Ser	Glu	Gln	Lys	Glu	Asn	
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Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	Gln	Asn	Thr	
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Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	
		100					105						110			
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Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu	
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Arg	Pro	Val	Glu	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	
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Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	
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Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	
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Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr	
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Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys	
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Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	
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Asp	Phe	Glu	Ala	Leu	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	
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Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys	
305					310					315					320	
tat	cct	cat	act	cat	ctg	gta	cac	caa	gca	aac	ccc	aga	ggg	tca	gca	1008
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	
				325					330					335		
ggc	cct	tgc	tgt	act	ccc	aca	aag	atg	tct	cca	att	aat	atg	cta	tat	1056
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	

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370 375

<210> 10  
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<212> PRT  
<213> Baboon

<40> 10

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Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His
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Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu
	145				150					155					160
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				165					170					175	
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu
			180					185					190		
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		195				200						205			
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly
	210					215					220				
Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr
	225				230					235					240
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys
				245					250					255	
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys
			260					265					270		
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val
		275					280					285			
Asp	Phe	Glu	Ala	Leu	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr
	290					295					300				
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys
	305				310					315					320
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala
				325					330					335	
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr
			340					345					350		
Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val
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gtt gct ggc cca gtg gat ctg aat gag aac agc gag cag aag gaa aat	96
Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn	
20 25 30	
gtg gaa aaa gag ggg ctg tgt aat gca tgt ttg tgg agg gaa aac act	144
Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Leu Trp Arg Glu Asn Thr	
35 40 45	
aca tcg tca aga cta gaa gcc ata aaa atc caa atc ctc agt aaa ctt	192
Thr Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu	
50 55 60	
cgc ctg gaa aca gct cct aac atc agc aaa gat gct atc aga caa ctt	240
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu	
65 70 75 80	
ttg ccc aag gct cct cca ctc ctg gaa ctg att gat cag ttc gat gtc	288
Leu Pro Lys Ala Pro Pro Leu Leu Glu Leu Ile Asp Gln Phe Asp Val	
85 90 95	
cag aga gat gcc agc agt gac ggc tcc ttg gaa gac gat gac tac cac	336
Gln Arg Asp Ala Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His	
100 105 110	
gcc agg acg gaa acg gtc att acc atg ccc acg gag tct gat ctt cta	384
Ala Arg Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu	
115 120 125	
acg caa gtg gaa gga aaa ccc aaa tgt tgc ttc ttt aaa ttt agc tct	432
Thr Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser	
130 135 140	
aag ata caa tac aat aaa cta gta aag gcc caa ctg tgg ata tat ctg	480
Lys Ile Gln Tyr Asn Lys Leu Val Lys Ala Gln Leu Trp Ile Tyr Leu	
145 150 155 160	
agg cct gtc aag act cct gcg aca gtg ttt gtg caa atc ctg aga ctc	528
Arg Pro Val Lys Thr Pro Ala Thr Val Phe Val Gln Ile Leu Arg Leu	
165 170 175	
atc aaa ccc atg aaa gac ggt aca agg tat act gga atc cga tct ctg	576
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu	
180 185 190	
aaa ctt gac atg aac cca ggc act ggt att tgg cag agc att gat gtg	624
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val	
195 200 205	



aag aca gtg ttg cag aac tgg ctc aaa caa cct gaa tcc aac tta ggc	672
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly	
210 215 220	
att gaa atc aaa gct tta gat gag aat ggc cat gat ctt gct gta acc	720
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr	
225 230 235 240	
ttc cca gaa cca gga gaa gat gga ctg act ccc ttt tta gaa gtc aag	768
Phe Pro Glu Pro Gly Glu Asp Gly Leu Thr Pro Phe Leu Glu Val Lys	
245 250 255	
gta aca gac aca cca aaa aga tct agg aga gat ttt ggg ctt gat tgt	816
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys	
260 265 270	
gat gaa cac tcc aca gaa tct cga tgc tgt cgt tac cct cta act gtg	864
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val	
275 280 285	
gat ttt gaa gct ttt gga tgg gat tgg att att gca cct aaa aga tat	912
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr	
290 295 300	
aag gcc aat tac tgc tct gga gaa tgt gaa ttt gta ttt ttg caa aag	960
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys	
305 310 315 320	
tat cct cat acc cat ctt gtg cac caa gca aac ccc aga ggt tca gcc	1008
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala	
325 330 335	
ggc ccc tgc tgt act cct aca aag atg tct cca att aat atg cta tat	1056
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr	
340 345 350	
ttt aat ggc gaa gga caa ata ata tac ggg aag att cca gcc atg gta	1104
Phe Asn Gly Glu Gly Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val	
355 360 365	
gta gat cgc tgt ggg tgt tca tga	1128
Val Asp Arg Cys Gly Cys Ser	
370 375	

&lt;210&gt; 12

&lt;211&gt; 375

&lt;212&gt; PRT

&lt;213&gt; Bovine

&lt;400&gt; 12

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Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn	
20 25 30	
Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Leu Trp Arg Glu Asn Thr	
35 40 45	
Thr Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu	
50 55 60	

Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu  
 65 70 75 80  
 Leu Pro Lys Ala Pro Leu Leu Glu Leu Ile Asp Gln Phe Asp Val  
 85 90 95  
 Gln Arg Asp Ala Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His  
 100 105 110  
 Ala Arg Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu  
 115 120 125  
 Thr Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser  
 130 135 140  
 Lys Ile Gln Tyr Asn Lys Leu Val Lys Ala Gln Leu Trp Ile Tyr Leu  
 145 150 155 160  
 Arg Pro Val Lys Thr Pro Ala Thr Val Phe Val Gln Ile Leu Arg Leu  
 165 170 175  
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu  
 180 185 190  
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val  
 195 200 205  
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly  
 210 215 220  
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr  
 225 230 235 240  
 Phe Pro Glu Pro Gly Glu Asp Gly Leu Thr Pro Phe Leu Glu Val Lys  
 245 250 255  
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys  
 260 265 270  
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val  
 275 280 285  
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr  
 290 295 300  
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys  
 305 310 315 320  
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala  
 325 330 335  
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr  
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 370 375

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 <212> DNA  
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<220>  
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 1 5 10 15  
 gtt gct ggt ccc gtg gat ctg aat gag aac agc gag caa aag gaa aat 96  
 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn  
 20 25 30  
 gtg gaa aaa gag ggg ctg tgt aat gca tgt atg tgg aga caa aac act 144

Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Met	Trp	Arg	Gln	Asn	Thr	
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Lys	Ser	Ser	Arg	Leu	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	
		50				55					60					
cgc	ctg	gaa	aca	gct	cct	aac	att	agc	aaa	gat	gct	ata	aga	caa	ctt	240
Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu	
		65			70					75					80	
ttg	ccc	aaa	gct	cct	cca	ctc	cgg	gaa	ctg	att	gat	cag	tac	gat	gtc	288
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	
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cag	aga	gat	gac	agc	agt	gat	ggc	tcc	ttg	gaa	gat	gat	gat	tat	cac	336
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	
			100					105						110		
gct	acg	acg	gaa	acg	atc	att	acc	atg	cct	aca	gag	tct	gat	ctt	cta	384
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Leu	Leu	
			115				120					125				
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Met	Gln	Val	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	
		130				135					140					
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Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	
		145			150				155						160	
aga	ccc	gtc	aag	act	cct	aca	aca	gtg	ttt	gtg	caa	atc	ctg	aga	ctc	528
Arg	Pro	Val	Lys	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	
				165					170					175		
atc	aaa	ccc	atg	aaa	gac	ggc	aca	agg	tat	act	gga	atc	cga	tct	ctg	576
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	
			180					185					190			
aaa	ctt	gac	atg	aac	cca	ggc	act	ggc	att	tgg	cag	agc	att	gat	gtg	624
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	
		195					200					205				
aag	aca	gtg	ttg	caa	aat	tgg	ctc	aaa	caa	cct	gaa	tcc	aac	tta	ggc	672
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	
		210				215					220					
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Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr	
				225		230				235					240	
ttc	cca	gga	cca	gga	gaa	gat	ggg	ctg	aat	ccc	ttt	tta	gaa	gtc	aag	768
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys	
				245					250					255		
gta	aca	gac	aca	cca	aaa	aga	tcc	agg	aga	gat	ttt	gga	ctc	gac	tgt	816
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	
			260					265					270			
gat	gag	cac	tca	aca	gaa	tct	cga	tgc	tgt	cgt	tac	cct	cta	act	gtg	864

Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val		
		275					280					285					
gat	ttt	gaa	gct	ttt	gga	tgg	gac	tgg	att	att	gca	ccc	aaa	aga	tat		912
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr		
	290					295					300						
aag	gcc	aat	tac	tgc	tct	gga	gag	tgt	gaa	ttt	gta	ttt	tta	caa	aaa		960
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys		
	305				310					315					320		
tac	cct	cac	act	cat	ctt	gtg	cac	caa	gca	aac	ccc	aga	ggg	tca	gca		1008
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala		
				325					330					335			
ggc	ccc	tgc	tgt	act	ccc	aca	aag	atg	tct	cca	atc	aat	atg	cta	tat		1056
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr		
		340						345					350				
ttt	aat	ggc	aaa	gaa	caa	ata	ata	tat	ggg	aaa	att	cca	gcc	atg	gta		1104
Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val		
	355					360						365					
gta	gat	cgc	tgt	ggg	tgc	tca	tga										1128
Val	Asp	Arg	Cys	Gly	Cys	Ser											
	370					375											

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 <212> PRT  
 <213> Porcine

<400> 14

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Val	Ala	Gly	Pro	Val	Asp	Leu	Asn	Glu	Asn	Ser	Glu	Gln	Lys	Glu	Asn		
		20						25					30				
Val	Glu	Lys	Glu	Gly	Leu	Cys	Asn	Ala	Cys	Met	Trp	Arg	Gln	Asn	Thr		
		35					40					45					
Lys	Ser	Ser	Arg	Leu	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu		
	50					55				60							
Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu		
	65				70					75					80		
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val		
			85					90						95			
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His		
		100						105					110				
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Leu	Leu		
		115					120					125					
Met	Gln	Val	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser		
	130					135					140						
Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu		
	145				150					155					160		
Arg	Pro	Val	Lys	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu		
			165					170						175			
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu		
		180						185					190				
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val		
	195					200						205					

Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly  
 210 215 220  
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr  
 225 230 235 240  
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys  
 245 250 255  
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys  
 260 265 270  
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val  
 275 280 285  
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr  
 290 295 300  
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys  
 305 310 315 320  
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala  
 325 330 335  
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr  
 340 345 350  
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 Val Asp Arg Cys Gly Cys Ser  
 370 375

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 <212> DNA  
 <213> Ovine

<220>  
 <221> CDS  
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 gtt gct ggc cca gtg gat ctg aat gag aac agc gag cag aag gaa aat 96  
 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn  
 20 25 30  
 gtg gaa aaa aag ggg ctg tgt aat gca tgc ttg tgg aga caa aac aat 144  
 Val Glu Lys Lys Gly Leu Cys Asn Ala Cys Leu Trp Arg Gln Asn Asn  
 35 40 45  
 aaa tcc tca aga cta gaa gcc ata aaa atc caa atc ctc agt aag ctt 192  
 Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu  
 50 55 60  
 cgc ctg gaa aca gct cct aac atc agc aaa gat gct ata aga caa ctt 240  
 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu  
 65 70 75 80  
 ttg ccc aag gct cct cca ctc cgg gaa ctg att gat cag tac gat gtc 288  
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val  
 85 90 95  
 cag aga gat gac agc agc gac ggc tcc ttg gaa gac gat gac tac cac 336  
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His  
 100 105 110

gtt	acg	acg	gaa	acg	gtc	att	acc	atg	ccc	acg	gag	tct	gat	ctt	cta	384
Val	Thr	Thr	Glu	Thr	Val	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Leu	Leu	
		115					120					125				
gca	gaa	gtg	caa	gaa	aaa	ccc	aaa	tgt	tgc	ttc	ttt	aaa	ttt	agc	tct	432
Ala	Glu	Val	Gln	Glu	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	
	130					135					140					
aag	ata	caa	cac	aat	aaa	gta	gta	aag	gcc	caa	ctg	tgg	ata	tat	ctg	480
Lys	Ile	Gln	His	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	
	145				150				155						160	
aga	cct	gtc	aag	act	cct	aca	aca	gtg	ttt	gtg	caa	atc	ctg	aga	ctc	528
Arg	Pro	Val	Lys	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	
				165					170						175	
atc	aaa	ccc	atg	aaa	gac	ggc	aca	agg	tat	act	gga	atc	cga	tct	ctg	576
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	
			180					185					190			
aaa	ctt	gac	atg	aac	cca	ggc	act	ggc	att	tgg	cag	agc	att	gat	gtg	624
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	
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Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	
	210					215					220					
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Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr	
	225				230					235					240	
ttc	cca	gaa	cca	gga	gaa	gaa	gga	ctg	aat	cct	ttt	tta	gaa	gtc	aag	768
Phe	Pro	Glu	Pro	Gly	Glu	Glu	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys	
				245					250					255		
gta	aca	gac	aca	cca	aaa	aga	tct	agg	aga	gat	ttt	ggg	ctt	gat	tgt	816
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	
			260					265					270			
gat	gag	cac	tcc	aca	gaa	tct	cga	tgc	tgt	cgt	tac	cct	cta	act	gtg	864
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	
		275					280					285				
gat	ttt	gaa	gct	ttt	gga	tgg	gat	tgg	att	att	gca	cct	aaa	aga	tat	912
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	
	290					295					300					
aag	gcc	aat	tac	tgc	tct	gga	gaa	tgt	gaa	ttt	tta	ttt	ttg	caa	aag	960
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Leu	Phe	Leu	Gln	Lys	
	305				310					315					320	
tat	cct	cat	acc	cat	ctt	gtg	cac	caa	gca	aac	ccc	aaa	ggc	tca	gcc	1008
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Lys	Gly	Ser	Ala	
				325					330					335		
ggc	cct	tgc	tgt	act	cct	aca	aag	atg	tct	cca	att	aat	atg	cta	tat	1056
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	
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1104

1128

[illegible]

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Val	Ala	Gly	Pro	Val	Asp	Leu	Asn	Glu	Asn	Ser	Glu	Gln	Lys	Glu	Asn	
			20					25					30			
Val	Glu	Lys	Gly	Leu	Cys	Asn	Ala	Cys	Leu	Trp	Arg	Gln	Asn	Asn		
		35				40					45					
Lys	Ser	Ser	Arg	Leu	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	
	50					55				60						
Arg	Leu	Glu	Thr	Ala	Pro	Asn	Ile	Ser	Lys	Asp	Ala	Ile	Arg	Gln	Leu	
65					70					75					80	
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Arg	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	
				85					90					95		
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	
			100					105					110			
Val	Thr	Thr	Glu	Thr	Val	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Leu	Leu	
		115					120					125				
Ala	Glu	Val	Gln	Glu	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	
	130					135				140						
Lys	Ile	Gln	His	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	
145					150					155					160	
Arg	Pro	Val	Lys	Thr	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	
				165					170					175		
Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	
			180					185					190			
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	
		195				200					205					
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	
	210					215					220					
Ile	Glu	Ile	Lys	Ala	Leu	Asp	Glu	Asn	Gly	His	Asp	Leu	Ala	Val	Thr	
225					230					235					240	
Phe	Pro	Glu	Pro	Gly	Glu	Glu	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Lys	
				245					250					255		
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	
			260					265					270			
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	
		275					280					285				
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	
	290					295					300					
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Leu	Phe	Leu	Gln	Lys	
305					310					315					320	
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Lys	Gly	Ser	Ala	
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Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Gly Met Val  
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 Val Asp Arg Cys Gly Cys Ser  
 370 375

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<211> 1128

<212> DNA

<213> Meleagris gallopavo

<220>

<221> CDS

<222> (1)...(1125)

<400> 17

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1				5				10					15			
tta	gtt	cat	ccg	gtg	gct	ctt	gat	ggc	agt	agt	cag	ccc	aca	gag	aac	96
Leu	Val	His	Pro	Val	Ala	Leu	Asp	Gly	Ser	Ser	Gln	Pro	Thr	Glu	Asn	
			20					25					30			
gct	gaa	aaa	gac	gga	ctg	tgc	aat	gct	tgc	acg	tgg	aga	cag	aat	act	144
Ala	Glu	Lys	Asp	Gly	Leu	Cys	Asn	Ala	Cys	Thr	Trp	Arg	Gln	Asn	Thr	
		35					40					45				
aaa	tcc	tcc	aga	ata	gaa	gcc	ata	aaa	att	caa	atc	ctc	agc	aaa	ctg	192
Lys	Ser	Ser	Arg	Ile	Glu	Ala	Ile	Lys	Ile	Gln	Ile	Leu	Ser	Lys	Leu	
	50					55					60					
cgc	ctg	gaa	caa	gca	cct	aac	att	agc	agg	gac	gtt	att	aaa	caa	ctt	240
Arg	Leu	Glu	Gln	Ala	Pro	Asn	Ile	Ser	Arg	Asp	Val	Ile	Lys	Gln	Leu	
	65				70				75						80	
tta	ccc	aaa	gct	cct	ccg	ctg	cag	gaa	ctg	att	gat	cag	tat	gac	gtc	288
Leu	Pro	Lys	Ala	Pro	Pro	Leu	Gln	Glu	Leu	Ile	Asp	Gln	Tyr	Asp	Val	
				85				90						95		
cag	aga	gac	gac	agt	agc	gat	ggc	tct	ttg	gaa	gac	gat	gac	tat	cat	336
Gln	Arg	Asp	Asp	Ser	Ser	Asp	Gly	Ser	Leu	Glu	Asp	Asp	Asp	Tyr	His	
		100					105						110			
gcc	aca	acc	gaa	acg	att	atc	aca	atg	cct	acg	gag	tct	gat	ttt	ctt	384
Ala	Thr	Thr	Glu	Thr	Ile	Ile	Thr	Met	Pro	Thr	Glu	Ser	Asp	Phe	Leu	
		115					120					125				
gta	caa	atg	gag	gga	aaa	cca	aaa	tgt	tgc	ttc	ttt	aag	ttt	agc	tct	432
Val	Gln	Met	Glu	Gly	Lys	Pro	Lys	Cys	Cys	Phe	Phe	Lys	Phe	Ser	Ser	
	130					135					140					
aaa	ata	caa	tat	aac	aaa	gta	gta	aag	gca	caa	tta	tgg	ata	tac	ttg	480
Lys	Ile	Gln	Tyr	Asn	Lys	Val	Val	Lys	Ala	Gln	Leu	Trp	Ile	Tyr	Leu	
	145				150				155						160	
agg	caa	gtc	caa	aaa	cct	aca	acg	gtg	ttt	gtg	cag	atc	ctg	aga	ctc	528
Arg	Gln	Val	Gln	Lys	Pro	Thr	Thr	Val	Phe	Val	Gln	Ile	Leu	Arg	Leu	
				165				170						175		
att	aaa	ccc	atg	aaa	gac	ggt	aca	aga	tat	act	gga	att	cga	tct	ttg	576



Ile	Lys	Pro	Met	Lys	Asp	Gly	Thr	Arg	Tyr	Thr	Gly	Ile	Arg	Ser	Leu	
			180					185					190			
aaa	ctt	gac	atg	aac	cca	ggc	act	ggg	atc	tgg	cag	agt	att	gat	gtg	624
Lys	Leu	Asp	Met	Asn	Pro	Gly	Thr	Gly	Ile	Trp	Gln	Ser	Ile	Asp	Val	
		195					200					205				
aag	aca	gtg	ttg	caa	aat	tgg	ctc	aaa	cag	cct	gaa	tcc	aat	tta	ggc	672
Lys	Thr	Val	Leu	Gln	Asn	Trp	Leu	Lys	Gln	Pro	Glu	Ser	Asn	Leu	Gly	
	210					215					220					
atc	gaa	ata	aaa	gct	ttt	gat	gag	aat	gga	cga	gat	ctt	gct	gta	aca	720
Ile	Glu	Ile	Lys	Ala	Phe	Asp	Glu	Asn	Gly	Arg	Asp	Leu	Ala	Val	Thr	
225					230					235					240	
ttc	cca	gga	cca	ggg	gaa	gat	gga	ctg	aac	cca	ttt	tta	gag	gtc	aga	768
Phe	Pro	Gly	Pro	Gly	Glu	Asp	Gly	Leu	Asn	Pro	Phe	Leu	Glu	Val	Arg	
				245					250					255		
gtt	aca	gac	aca	cca	aaa	cgg	tcc	cgc	aga	gat	ttt	ggc	ctt	gac	tgc	816
Val	Thr	Asp	Thr	Pro	Lys	Arg	Ser	Arg	Arg	Asp	Phe	Gly	Leu	Asp	Cys	
			260					265					270			
gac	gag	cac	tca	acg	gaa	tct	cga	tgt	tgt	cgc	tac	ccg	ctg	aca	gtg	864
Asp	Glu	His	Ser	Thr	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	
		275					280					285				
gat	ttt	gaa	gct	ttt	gga	tgg	gac	tgg	att	ata	gca	cct	aaa	aga	tac	912
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	
	290					295					300					
aaa	gcc	aat	tac	tgc	tct	gga	gaa	tgt	gaa	ttc	gta	ttt	cta	cag	aaa	960
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Glu	Cys	Glu	Phe	Val	Phe	Leu	Gln	Lys	
305					310					315					320	
tac	ccg	cac	act	cac	ctg	gta	cac	caa	gca	aat	cca	aga	ggc	tca	gca	1008
Tyr	Pro	His	Thr	His	Leu	Val	His	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	
				325					330					335		
ggc	cct	tgc	tgc	aca	ccc	acc	aag	atg	tcc	cct	ata	aac	atg	ctg	tat	1056
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu	Tyr	
				340				345					350			
ttc	aat	gga	aaa	gaa	caa	ata	ata	tat	gga	aag	ata	cca	gcc	atg	gtt	1104
Phe	Asn	Gly	Lys	Glu	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Ala	Met	Val	
		355					360					365				
gta	gat	cgt	tgc	ggg	tgc	tca	tga									1128
Val	Asp	Arg	Cys	Gly	Cys	Ser										
		370				375										

&lt;210&gt; 18

&lt;211&gt; 375

&lt;212&gt; PRT

&lt;213&gt; Meleagris gallopavo

&lt;400&gt; 18

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Leu Val His Pro Val Ala Leu Asp Gly Ser Ser Gln Pro Thr Glu Asn  
 20 25 30  
 Ala Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr  
 35 40 45  
 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu  
 50 55 60  
 Arg Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile Lys Gln Leu  
 65 70 75 80  
 Leu Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln Tyr Asp Val  
 85 90 95  
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His  
 100 105 110  
 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu  
 115 120 125  
 Val Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser  
 130 135 140  
 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu  
 145 150 155 160  
 Arg Gln Val Gln Lys Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu  
 165 170 175  
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu  
 180 185 190  
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val  
 195 200 205  
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly  
 210 215 220  
 Ile Glu Ile Lys Ala Phe Asp Glu Asn Gly Arg Asp Leu Ala Val Thr  
 225 230 235 240  
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg  
 245 250 255  
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys  
 260 265 270  
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val  
 275 280 285  
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr  
 290 295 300  
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys  
 305 310 315 320  
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala  
 325 330 335  
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr  
 340 345 350  
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val  
 355 360 365  
 Val Asp Arg Cys Gly Cys Ser  
 370 375

<210> 19  
 <211> 1125  
 <212> DNA  
 <213> Danio rerio

<220>  
 <221> CDS  
 <222> (1)...(1122)

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 Met His Phe Thr Gln Val Leu Ile Ser Leu Ser Val Leu Ile Ala Cys  
 1 5 10 15

ggt cca gtg ggt tat gga gat ata acg gcg cac cag cag cct tcc aca	96
Gly Pro Val Gly Tyr Gly Asp Ile Thr Ala His Gln Gln Pro Ser Thr	
20 25 30	
gcc acg gag gaa agc gag ctg tgt tcc aca tgt gag ttc aga caa cac	144
Ala Thr Glu Glu Ser Glu Leu Cys Ser Thr Cys Glu Phe Arg Gln His	
35 40 45	
agc aag ctg atg aga ctg cat gcc atc aag tcc caa att ctt agc aaa	192
Ser Lys Leu Met Arg Leu His Ala Ile Lys Ser Gln Ile Leu Ser Lys	
50 55 60	
ctc cga ctc aag cag gct cca aac atc agc cgg gac gtg gtc aag cag	240
Leu Arg Leu Lys Gln Ala Pro Asn Ile Ser Arg Asp Val Val Lys Gln	
65 70 75 80	
ctg tta ccc aaa gca ccg cct ttg caa caa ctt ctg gat cag tac gat	288
Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln Leu Leu Asp Gln Tyr Asp	
85 90 95	
gtt tta gga gat gac agt aag gat gga gct gtg gaa gag gac gat gaa	336
Val Leu Gly Asp Asp Ser Lys Asp Gly Ala Val Glu Glu Asp Asp Glu	
100 105 110	
cat gcc acc aca gag acc atc atg acc atg gcc aca gaa cct gac ccc	384
His Ala Thr Thr Glu Thr Ile Met Thr Met Ala Thr Glu Pro Asp Pro	
115 120 125	
att gtt caa gta gat cgg aaa ccg aag tgt tgc ttt ttc tcc ttc agt	432
Ile Val Gln Val Asp Arg Lys Pro Lys Cys Cys Phe Phe Ser Phe Ser	
130 135 140	
ccg aag atc caa gcg aac ccg atc gta aga gcg cag ctc tgg gtt cat	480
Pro Lys Ile Gln Ala Asn Arg Ile Val Arg Ala Gln Leu Trp Val His	
145 150 155 160	
ctg aga ccg gcg gag gag gcg acc acc gtc ttc tta cag ata tct cgg	528
Leu Arg Pro Ala Glu Glu Ala Thr Thr Val Phe Leu Gln Ile Ser Arg	
165 170 175	
ctg atg ccc gtt aag gac gga gga aga cac cga ata cga tcc ctg aaa	576
Leu Met Pro Val Lys Asp Gly Gly Arg His Arg Ile Arg Ser Leu Lys	
180 185 190	
atc gac gtg aac gca gga gtc acg tct tgg cag agt ata gac gta aag	624
Ile Asp Val Asn Ala Gly Val Thr Ser Trp Gln Ser Ile Asp Val Lys	
195 200 205	
cag gtg ctc acg gtg tgg tta aaa caa ccg gag acc aac cga ggc atc	672
Gln Val Leu Thr Val Trp Leu Lys Gln Pro Glu Thr Asn Arg Gly Ile	
210 215 220	
gag att aac gca tat gac gcg aag gga aac gac ttg gcc gtc act tca	720
Glu Ile Asn Ala Tyr Asp Ala Lys Gly Asn Asp Leu Ala Val Thr Ser	
225 230 235 240	
acc gag act ggg gag gat gga ctg ctc ccc ttt atg gag gtg aaa ata	768
Thr Glu Thr Gly Glu Asp Gly Leu Leu Pro Phe Met Glu Val Lys Ile	
245 250 255	

tca gag ggc cca aaa cga atc cgg agg gac tcc gga ctg gac tgc gat 816  
 Ser Glu Gly Pro Lys Arg Ile Arg Arg Asp Ser Gly Leu Asp Cys Asp  
                   260                  265                  270

gag aat tcc tca gag tct cgc tgc tgc agg tac cct ctc act gtg gac 864  
 Glu Asn Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp  
                   275                  280                  285

ttc gag gac ttt ggc tgg gac tgg att att gct cca aaa cgc tat aag 912  
 Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys  
                   290                  295                  300

gcg aat tac tgt tca gga gaa tgc gac tac atg tac ctg cag aag tat 960  
 Ala Asn Tyr Cys Ser Gly Glu Cys Asp Tyr Met Tyr Leu Gln Lys Tyr  
                   305                  310                  315                  320

ccc cac acc cat ctg gtg aac aag gcc agt ccg aga gga acg gct ggg 1008  
 Pro His Thr His Leu Val Asn Lys Ala Ser Pro Arg Gly Thr Ala Gly  
                   325                  330                  335

ccc tgc tgc act ccc acc aag atg tct ccc atc aac atg ctt tac ttt 1056  
 Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe  
                   340                  345                  350

aac ggc aaa gag cag atc atc tac ggc aag atc cct tcg atg gta gta 1104  
 Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met Val Val  
                   355                  360                  365

gac cgc tgt ggc tgc tca tga 1125  
 Asp Arg Cys Gly Cys Ser  
                   370

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<211> 374

<212> PRT

<213> Danio rerio

<400> 20

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                   20                  25                  30  
 Ala Thr Glu Ser Glu Leu Cys Ser Thr Cys Glu Phe Arg Gln His  
                   35                  40                  45  
 Ser Lys Leu Met Arg Leu His Ala Ile Lys Ser Gln Ile Leu Ser Lys  
                   50                  55                  60  
 Leu Arg Leu Lys Gln Ala Pro Asn Ile Ser Arg Asp Val Val Lys Gln  
   65                  70                  75                  80  
 Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln Leu Leu Asp Gln Tyr Asp  
                   85                  90                  95  
 Val Leu Gly Asp Asp Ser Lys Asp Gly Ala Val Glu Glu Asp Asp Glu  
                   100                  105                  110  
 His Ala Thr Thr Glu Thr Ile Met Thr Met Ala Thr Glu Pro Asp Pro  
                   115                  120                  125  
 Ile Val Gln Val Asp Arg Lys Pro Lys Cys Cys Phe Phe Ser Phe Ser  
                   130                  135                  140  
 Pro Lys Ile Gln Ala Asn Arg Ile Val Arg Ala Gln Leu Trp Val His  
   145                  150                  155                  160

Leu Arg Pro Ala Glu Glu Ala Thr Thr Val Phe Leu Gln Ile Ser Arg  
                     165                    170                    175  
 Leu Met Pro Val Lys Asp Gly Gly Arg His Arg Ile Arg Ser Leu Lys  
                     180                    185                    190  
 Ile Asp Val Asn Ala Gly Val Thr Ser Trp Gln Ser Ile Asp Val Lys  
                     195                    200                    205  
 Gln Val Leu Thr Val Trp Leu Lys Gln Pro Glu Thr Asn Arg Gly Ile  
                     210                    215                    220  
 Glu Ile Asn Ala Tyr Asp Ala Lys Gly Asn Asp Leu Ala Val Thr Ser  
 225                    230                    235                    240  
 Thr Glu Thr Gly Glu Asp Gly Leu Leu Pro Phe Met Glu Val Lys Ile  
                     245                    250                    255  
 Ser Glu Gly Pro Lys Arg Ile Arg Arg Asp Ser Gly Leu Asp Cys Asp  
                     260                    265                    270  
 Glu Asn Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp  
                     275                    280                    285  
 Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys  
                     290                    295                    300  
 Ala Asn Tyr Cys Ser Gly Glu Cys Asp Tyr Met Tyr Leu Gln Lys Tyr  
 305                    310                    315                    320  
 Pro His Thr His Leu Val Asn Lys Ala Ser Pro Arg Gly Thr Ala Gly  
                     325                    330                    335  
 Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe  
                     340                    345                    350  
 Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met Val Val  
                     355                    360                    365  
 Asp Arg Cys Gly Cys Ser  
                     370

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<213> Artificial Sequence

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<223> proteolytic cleavage site

<221> VARIANT

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<223> Xaa = Any Amino Acid

<400> 21

Arg Xaa Xaa Arg

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<223> proteolytic processing site

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Arg Ser Arg Arg

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 Met  
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gtg ctc gcg gcc ccg ctg ctg ctg ggc ttc ctg ctc ctc gcc ctg gag 104  
 Val Leu Ala Ala Pro Leu Leu Leu Gly Phe Leu Leu Leu Ala Leu Glu  
 5 10 15

ctg cgg ccc cgg ggg gag gcg gcc gag ggc ccc gcg gcg gcg gcg gcg 152  
 Leu Arg Pro Arg Gly Glu Ala Ala Glu Gly Pro Ala Ala Ala Ala Ala  
 20 25 30

gcg gcg gcg gcg gcg gca gcg gcg ggg gtc ggg ggg gag cgc tcc agc 200  
 Ala Ala Ala Ala Ala Ala Ala Ala Ala Gly Val Gly Gly Glu Arg Ser Ser  
 35 40 45

cgg cca gcc ccg tcc gtg gcg ccc gag ccg gac ggc tgc ccc gtg tgc 248  
 Arg Pro Ala Pro Ser Val Ala Pro Glu Pro Asp Gly Cys Pro Val Cys  
 50 55 60 65

gtt tgg cgg cag cac agc cgc gag ctg cgc cta gag agc atc aag tcg 296  
 Val Trp Arg Gln His Ser Arg Glu Leu Arg Leu Glu Ser Ile Lys Ser  
 70 75 80

cag atc ttg agc aaa ctg cgg ctc aag gag gcg ccc aac atc agc cgc 344  
 Gln Ile Leu Ser Lys Leu Arg Leu Lys Glu Ala Pro Asn Ile Ser Arg  
 85 90 95

gag gtg gtg aag cag ctg ctg ccc aag gcg ccg ccg ctg cag cag atc 392  
 Glu Val Val Lys Gln Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln Ile  
 100 105 110

ctg gac cta cac gac ttc cag ggc gac gcg ctg cag ccc gag gac ttc 440  
 Leu Asp Leu His Asp Phe Gln Gly Asp Ala Leu Gln Pro Glu Asp Phe  
 115 120 125

ctg	gag	gag	gac	gag	tac	cac	gcc	acc	acc	gag	acc	gtc	att	agc	atg	488
Leu	Glu	Glu	Asp	Glu	Tyr	His	Ala	Thr	Thr	Glu	Thr	Val	Ile	Ser	Met	
130					135					140					145	
gcc	cag	gag	acg	gac	cca	gca	gta	cag	aca	gat	ggc	agc	cct	ctc	tgc	536
Ala	Gln	Glu	Thr	Asp	Pro	Ala	Val	Gln	Thr	Asp	Gly	Ser	Pro	Leu	Cys	
				150						155					160	
tgc	cat	ttt	cac	ttc	agc	ccc	aag	gtg	atg	ttc	aca	aag	gta	ctg	aag	584
Cys	His	Phe	His	Phe	Ser	Pro	Lys	Val	Met	Phe	Thr	Lys	Val	Leu	Lys	
			165						170					175		
gcc	cag	ctg	tgg	gtg	tac	cta	cgg	cct	gta	ccc	cgc	cca	gcc	aca	gtc	632
Ala	Gln	Leu	Trp	Val	Tyr	Leu	Arg	Pro	Val	Pro	Arg	Pro	Ala	Thr	Val	
		180					185						190			
tac	ctg	cag	atc	ttg	cga	cta	aaa	ccc	cta	act	ggg	gaa	ggg	acc	gca	680
Tyr	Leu	Gln	Ile	Leu	Arg	Leu	Lys	Pro	Leu	Thr	Gly	Glu	Gly	Thr	Ala	
	195					200					205					
ggg	gga	ggg	ggc	gga	ggc	cgg	cgt	cac	atc	cgt	atc	cgc	tca	ctg	aag	728
Gly	Gly	Gly	Gly	Gly	Gly	Arg	Arg	His	Ile	Arg	Ile	Arg	Ser	Leu	Lys	
210					215					220					225	
att	gag	ctg	cac	tca	cgc	tca	ggc	cat	tgg	cag	agc	atc	gac	ttc	aag	776
Ile	Glu	Leu	His	Ser	Arg	Ser	Gly	His	Trp	Gln	Ser	Ile	Asp	Phe	Lys	
				230					235					240		
caa	gtg	cta	cac	agc	tgg	ttc	cgc	cag	cca	cag	agc	aac	tgg	ggc	atc	824
Gln	Val	Leu	His	Ser	Trp	Phe	Arg	Gln	Pro	Gln	Ser	Asn	Trp	Gly	Ile	
				245				250					255			
gag	atc	aac	gcc	ttt	gat	ccc	agt	ggc	aca	gac	ctg	gct	gtc	acc	tcc	872
Glu	Ile	Asn	Ala	Phe	Asp	Pro	Ser	Gly	Thr	Asp	Leu	Ala	Val	Thr	Ser	
		260					265					270				
ctg	ggg	cgg	gga	gcc	gag	ggg	ctg	cat	cca	ttc	atg	gag	ctt	cga	gtc	920
Leu	Gly	Pro	Gly	Ala	Glu	Gly	Leu	His	Pro	Phe	Met	Glu	Leu	Arg	Val	
	275					280					285					
cta	gag	aac	aca	aaa	cgt	tcc	cgg	cgg	aac	ctg	ggg	ctg	gac	tgc	gac	968
Leu	Glu	Asn	Thr	Lys	Arg	Ser	Arg	Arg	Asn	Leu	Gly	Leu	Asp	Cys	Asp	
	290				295					300					305	
gag	cac	tca	agc	gag	tcc	cgc	tgc	tgc	cga	tat	ccc	ctc	aca	gtg	gac	1016
Glu	His	Ser	Ser	Glu	Ser	Arg	Cys	Cys	Arg	Tyr	Pro	Leu	Thr	Val	Asp	
				310					315					320		
ttt	gag	gct	ttc	ggc	tgg	gac	tgg	atc	atc	gca	cct	aag	cgc	tac	aag	1064
Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg	Tyr	Lys	
			325					330					335			
gcc	aac	tac	tgc	tcc	ggc	cag	tgc	gag	tac	atg	ttc	atg	caa	aaa	tat	1112
Ala	Asn	Tyr	Cys	Ser	Gly	Gln	Cys	Glu	Tyr	Met	Phe	Met	Gln	Lys	Tyr	
		340					345					350				
ccg	cat	acc	cat	ttg	gtg	cag	cag	gcc	aat	cca	aga	ggc	tct	gct	ggg	1160
Pro	His	Thr	His	Leu	Val	Gln	Gln	Ala	Asn	Pro	Arg	Gly	Ser	Ala	Gly	
	355					360					365					

ccc tgt tgt acc ccc acc aag atg tcc cca atc aac atg ctc tac ttc 1208  
 Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe  
 370 375 380 385

aat gac aag cag cag att atc tac ggc aag atc cct ggc atg gtg gtg 1256  
 Asn Asp Lys Gln Gln Ile Ile Tyr Gly Lys Ile Pro Gly Met Val Val  
 390 395 400

gat cgc tgt ggc tgc tct taagtgggtc actacaagct gctggagcaa 1304  
 Asp Arg Cys Gly Cys Ser  
 405

agacttggtg ggtgggtaac ttaacctctt cacagaggat aaaaaatgct tgtgagtatg 1364  
 acagaaggga ataaacaggc ttaaagggt 1393

<210> 25

<211> 407

<212> PRT

<213> Homo sapiens

<400> 25

Met Val Leu Ala Ala Pro Leu Leu Leu Gly Phe Leu Leu Leu Ala Leu  
 1 5 10 15  
 Glu Leu Arg Pro Arg Gly Glu Ala Ala Glu Gly Pro Ala Ala Ala Ala  
 20 25 30  
 Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Gly Val Gly Gly Glu Arg Ser  
 35 40 45  
 Ser Arg Pro Ala Pro Ser Val Ala Pro Glu Pro Asp Gly Cys Pro Val  
 50 55 60  
 Cys Val Trp Arg Gln His Ser Arg Glu Leu Arg Leu Glu Ser Ile Lys  
 65 70 75 80  
 Ser Gln Ile Leu Ser Lys Leu Arg Leu Lys Glu Ala Pro Asn Ile Ser  
 85 90 95  
 Arg Glu Val Val Lys Gln Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln  
 100 105 110  
 Ile Leu Asp Leu His Asp Phe Gln Gly Asp Ala Leu Gln Pro Glu Asp  
 115 120 125  
 Phe Leu Glu Glu Asp Glu Tyr His Ala Thr Thr Glu Thr Val Ile Ser  
 130 135 140  
 Met Ala Gln Glu Thr Asp Pro Ala Val Gln Thr Asp Gly Ser Pro Leu  
 145 150 155 160  
 Cys Cys His Phe His Phe Ser Pro Lys Val Met Phe Thr Lys Val Leu  
 165 170 175  
 Lys Ala Gln Leu Trp Val Tyr Leu Arg Pro Val Pro Arg Pro Ala Thr  
 180 185 190  
 Val Tyr Leu Gln Ile Leu Arg Leu Lys Pro Leu Thr Gly Glu Gly Thr  
 195 200 205  
 Ala Gly Gly Gly Gly Gly Arg Arg His Ile Arg Ile Arg Ser Leu  
 210 215 220  
 Lys Ile Glu Leu His Ser Arg Ser Gly His Trp Gln Ser Ile Asp Phe  
 225 230 235 240  
 Lys Gln Val Leu His Ser Trp Phe Arg Gln Pro Gln Ser Asn Trp Gly  
 245 250 255  
 Ile Glu Ile Asn Ala Phe Asp Pro Ser Gly Thr Asp Leu Ala Val Thr  
 260 265 270  
 Ser Leu Gly Pro Gly Ala Glu Gly Leu His Pro Phe Met Glu Leu Arg  
 275 280 285  
 Val Leu Glu Asn Thr Lys Arg Ser Arg Arg Asn Leu Gly Leu Asp Cys  
 290 295 300  
 Asp Glu His Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val



305					310					315				320
Asp	Phe	Glu	Ala	Phe	Gly	Trp	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Arg
				325					330					335
Lys	Ala	Asn	Tyr	Cys	Ser	Gly	Gln	Cys	Glu	Tyr	Met	Phe	Met	Gln
			340					345					350	
Tyr	Pro	His	Thr	His	Leu	Val	Gln	Gln	Ala	Asn	Pro	Arg	Gly	Ser
		355					360				365			
Gly	Pro	Cys	Cys	Thr	Pro	Thr	Lys	Met	Ser	Pro	Ile	Asn	Met	Leu
		370				375					380			
Phe	Asn	Asp	Lys	Gln	Gln	Ile	Ile	Tyr	Gly	Lys	Ile	Pro	Gly	Met
385					390					395				400
Val	Asp	Arg	Cys	Gly	Cys	Ser								
				405										

<210> 26  
 <211> 476  
 <212> DNA  
 <213> Salmon-1

<220>  
 <221> CDS  
 <222> (3)...(473)

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Gln Pro Glu Thr Asn Trp Gly Ile Glu Ile Asn Ala Phe Asp Ser	
1 5 10 15	
aag gga aat gat ctg gcc gtt acc tca gca gaa gcg gga gaa gga ctg	95
Lys Gly Asn Asp Leu Ala Val Thr Ser Ala Glu Ala Gly Glu Gly Leu	
20 25 30	
caa ccc ttc atg gag gtg acg att tca gag ggc ccg aag cgc tcc agg	143
Gln Pro Phe Met Glu Val Thr Ile Ser Glu Gly Pro Lys Arg Ser Arg	
35 40 45	
aga gac tcg ggc ctg gac tgt gac gag aac tcc ccc gag tcc cgc tgt	191
Arg Asp Ser Gly Leu Asp Cys Asp Glu Asn Ser Pro Glu Ser Arg Cys	
50 55 60	
tgc cgc tac ccc ctc acg gta gac ttt gaa gac ttt ggc tgg gac tgg	239
Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu Asp Phe Gly Trp Asp Trp	
65 70 75	
att att gcc ccc aag cgc tac aag gcc aac tac tgc tct ggt gag tgt	287
Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys	
80 85 90 95	
gag tac atg cac ctg cag aag tac ccc cac acc cac ctg gtg aac aag	335
Glu Tyr Met His Leu Gln Lys Tyr Pro His Thr His Leu Val Asn Lys	
100 105 110	
gct aac cct cgc ggc acc gca ggg ccc tgc tgc acc ccc acc aag atg	383
Ala Asn Pro Arg Gly Thr Ala Gly Pro Cys Cys Thr Pro Thr Lys Met	
115 120 125	
tcc ccc atc aac atg ctc tac ttc aac cgc aaa gag cag atc atc tac	431
Ser Pro Ile Asn Met Leu Tyr Phe Asn Arg Lys Glu Gln Ile Ile Tyr	
130 135 140	

ggc aag atc ccc tcc atg gtg gtg gac cgt tgc gga tgc tcg  
 Gly Lys Ile Pro Ser Met Val Val Asp Arg Cys Gly Cys Ser  
 145 150 155

473

tga

476

<210> 27  
 <211> 157  
 <212> PRT  
 <213> Salmon-1

<400> 27  
 Gln Pro Glu Thr Asn Trp Gly Ile Glu Ile Asn Ala Phe Asp Ser Lys  
 1 5 10 15  
 Gly Asn Asp Leu Ala Val Thr Ser Ala Glu Ala Gly Glu Gly Leu Gln  
 20 25 30  
 Pro Phe Met Glu Val Thr Ile Ser Glu Gly Pro Lys Arg Ser Arg Arg  
 35 40 45  
 Asp Ser Gly Leu Asp Cys Asp Glu Asn Ser Pro Glu Ser Arg Cys Cys  
 50 55 60  
 Arg Tyr Pro Leu Thr Val Asp Phe Glu Asp Phe Gly Trp Asp Trp Ile  
 65 70 75 80  
 Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu  
 85 90 95  
 Tyr Met His Leu Gln Lys Tyr Pro His Thr His Leu Val Asn Lys Ala  
 100 105 110  
 Asn Pro Arg Gly Thr Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser  
 115 120 125  
 Pro Ile Asn Met Leu Tyr Phe Asn Arg Lys Glu Gln Ile Ile Tyr Gly  
 130 135 140  
 Lys Ile Pro Ser Met Val Asp Arg Cys Gly Cys Ser  
 145 150 155

<210> 28  
 <211> 412  
 <212> DNA  
 <213> Salmon-2

<220>  
 <221> CDS  
 <222> (2)...(409)

<400> 28  
 g gtt acc tca act gaa gcc gga gaa gga ctg caa ccc ttc atg gag gtg  
 Val Thr Ser Thr Glu Ala Gly Glu Gly Leu Gln Pro Phe Met Glu Val  
 1 5 10 15

49

aag att tcg gag ggc ccg aag cgc tcc agg aga gat tcg ggc ctg gac  
 Lys Ile Ser Glu Gly Pro Lys Arg Ser Arg Arg Asp Ser Gly Leu Asp  
 20 25 30

97

tgt gat gag aac tcc ccc gag tcc cgc tgc tgc cgg tac ccc ctc acg  
 Cys Asp Glu Asn Ser Pro Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr  
 35 40 45

145

gtg gac ttt gaa gac ttt ggc tgg gac tgg att att gcc ccc aag cgc  
 Val Asp Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg  
 50 55 60

193

tac aag gcc aac tac tgc tct ggt gag tgc gag tac atg cac ctg cag

241

Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Tyr Met His Leu Gln  
 65 70 75 80

aag tac ccc cac acc cac ctg gtg aac aag gct aac cct cgc ggc acc 289  
 Lys Tyr Pro His Thr His Leu Val Asn Lys Ala Asn Pro Arg Gly Thr  
 85 90 95

gcg ggg ccc tgc tgc acc ccc acc aag atg tcc ccc atc aac atg ctc 337  
 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu  
 100 105 110

tac ttc aac cgc aaa gag cag atc atc tac ggc aag atc ccc tcc atg 385  
 Tyr Phe Asn Arg Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met  
 115 120 125

gtg gtg gac cgc tgc ggc tgc tcg tga 412  
 Val Val Asp Arg Cys Gly Cys Ser  
 130 135

<210> 29

<211> 136

<212> PRT

<213> Salmon-2

<400> 29

Val Thr Ser Thr Glu Ala Gly Glu Gly Leu Gln Pro Phe Met Glu Val  
 1 5 10 15  
 Lys Ile Ser Glu Gly Pro Lys Arg Ser Arg Arg Asp Ser Gly Leu Asp  
 20 25 30  
 Cys Asp Glu Asn Ser Pro Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr  
 35 40 45  
 Val Asp Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg  
 50 55 60  
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Tyr Met His Leu Gln  
 65 70 75 80  
 Lys Tyr Pro His Thr His Leu Val Asn Lys Ala Asn Pro Arg Gly Thr  
 85 90 95  
 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu  
 100 105 110  
 Tyr Phe Asn Arg Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met  
 115 120 125  
 Val Val Asp Arg Cys Gly Cys Ser  
 130 135